

QY 298 CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTTCATCAGAGATGAATTGTGACAGCGC 357  
DB 327 CGCTGTTAGAGAAAGTCTTCCAGTACATTGACCTTCATCAGAGATGAATTGTGACAGCGC 386  
QY 358 TGAAGGAGTGGTGGCCCATCAGAGCGGACTGTGTCCAGCCCTGTGCTTCCAGACAAG 417  
DB 387 TGAAGGAGTGGTGGCCCATCAGAGCGGACTGTGTCCAGCCCTGTGCTTCCAGACAAG 446  
QY 418 AGCTCTTCAGAGATGATGGCCGCTGCGGACACCGCTGCAGCGCCCTGGGGGGCCGCTGTGG 477  
DB 447 AGCTCTTCAGAGATGATGGCCGCTGCGGACACCGCTGCAGCGCCCTGGGGGGCCGCTGTGG 506  
QY 478 CCTCGGTGACATGGGTCTCTCAGCAGCTGCCCGATGCTCAGAGTCTTCCATACTCTCCCG 537  
DB 507 CCTCGGTGACATGGGTCTCTCAGCAGCTGCCCGATGCTCAGAGTCTTCCATACTCTCCCG 566  
QY 538 TCATCCTGGCCGAACTG 554  
DB 567 TCATCCTGGCCGAACTG 583

RESULT 2

US-09-513-999C-13950  
; Sequence 13950 Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Dumas Milne Edwards, J.B.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13950  
; LENGTH: 300  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 7  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 67  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 68  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 69  
; OTHER INFORMATION: m=a or c  
US-09-513-999C-13950

Query Match 8.0%; Score 180; DB 4; Length 300;  
Best Local Similarity 99.6%; Pred. No. 4.5e-66;  
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 66 TTCCTTCCGGGCAACGTTGGTCAAGGACAGAGATATTAATGTACCCCTCTTG 125  
DB 70 TTCCTTCCGGGCAACGTTGGTCAAGGACAGAGATATTAATGTACCCCTCTTG 129  
QY 126 GGCTTTTCATGGAAGTCTCCCTCTGCAATTTTGGAGGTTGGAAAGTTGCTAGAGGCTT 185  
DB 130 GGCTTTTCATGGAAGTCTCCCTCTGCAATTTTGGAGGTTGGAAAGTTGCTAGAGGCTT 189  
QY 186 CAGAACTCCAGCTTAATGATCCCAAATCGGAGAAATGGCTGCTGCTGCTGCTGTG 245

DB 190 CAGAACTCCAGCTTAATGATCCCAAATCGGAGAAATGGCTGCTGCTGCTGTG 249  
QY 246 CTGCTGCTGCTGCTGAGAGCGCGCATGTTCTCTCACCCTCCCGCCCGCG 296  
DB 250 CTGCTGCTGCTGCTGAGAGCGCGCATGTTCTCTCACCCTCCCGCCCGCG 300

RESULT 3

US-09-073-569-1  
; Sequence 1 Application US/09073569  
; Patent No. 6084088  
; GENERAL INFORMATION:  
; APPLICANT: Shepard, Paul O  
; APPLICANT: Grossmann, Angelika  
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZymoGenetics, Inc.  
; STREET: 1201 Eastlake Avenue East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/073,569  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sawislak, Deborah A  
; REGISTRATION NUMBER: 37,438  
; REFERENCE/DOCKET NUMBER: 97-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6672  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1733 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 34...1344  
; OTHER INFORMATION:  
US-09-073-569-1

Query Match 2.7%; Score 61; DB 3; Length 1733;  
Best Local Similarity 100.0%; Pred. No. 2.9e-16;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2182 CTCCTCAA 2241  
DB 1603 CTCCTCAA 1662  
QY 2242 A 2242  
DB 1663 A 1663

RESULT 4  
US-09-621-976-8550  
; Sequence 8550, Application US/09621976  
; Patent No. 6639063

~~US-10-036-342-56-18E~~

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLM11431 row: 9 column: 18  
High quality sequence stop: 701.

VERSION  
KEYWORDS  
SOURCE

JOURNAL	AUTHOR	TITLE	REFERENCE	ORGANIZATION
COMMENT				

0;	
TT 276	
TT 106	
CC 336	
CC 166	
CC 396	
CC 226	
CC 456	
CC 286	
CC 516	
CC 346	
AA 576	
AA 406	
AA 636	
AA 466	
FEATURES	
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Query Match 25.4%; Score 576; DB 1; Length 742;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-270;  
 Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1288 CAGTCATACCTGGCCGAGTTATAGAAATTTTCAATCCGCTAGTCCCTCAGCATGATG 1347  
 DB 609 CAGTCATACCTGGCCGAGTTATAGAAATTTTCAATCCGCTAGTCCCTCAGCATGATG 550  
 QY 1348 TGTCTGCGGTGGAATAAAGAGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATA 1407  
 DB 549 TGTCTGCGGTGGAATAAAGAGTGACACGACATCTTGAAGATGTGTTCTCCAAAAGAAATA 490  
 QY 1408 GTTCCAAACAGATGTTGTTTCCATGACTCTAGAGCTACACCCGCTGGATTGCAATATTG 1467  
 DB 489 GTTCCAAACAGATGTTGTTTCCATGACTCTAGAGCTACACCCGCTGGATTGCAATATTG 430  
 QY 1468 ATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGACAGTGTGTTGAAACAGAACCCAG 1527  
 DB 429 ATGACACCCAGTATCTCGCAGCAAAAAGAGCGATCAGACAGTGTGTTGAAACAGAACCCAG 370  
 QY 1528 ATATGATCCGGATGATGCCACCAATTCATTTGCCAAAATGTTCCAGAGAGATGTTCCACA 1587  
 DB 369 ATATGATCCGGATGATGCCACCAATTCATTTGCCAAAATGTTCCAGAGAGATGTTCCACA 310  
 QY 1588 AGAGCGTGTGCTAATTTCCGCTGGAGCTGTGATGATGAGAAATTCGTCAGATGAGA 1647  
 DB 309 AGAGCGTGTGCTAATTTCCGCTGGAGCTGTGATGATGAGAAATTCGTCAGATGAGA 250  
 QY 1648 AAATCAACAGGTGGAATACATAGAGGAAACCAATTTATTGCTGCTTTTCTTAGAGA 1707  
 DB 249 AAATCAACAGGTGGAATACATAGAGGAAACCAATTTATTGCTGCTTTTCTTAGAGA 190  
 QY 1708 TGGCCCGAGCTCCATTAATCAACAAGAACCTTCTAGTCTGATCCAGTCAAGATTTCA 1767  
 DB 189 TGGCCCGAGCTCCATTAATCAACAAGAACCTTCTAGTCTGATCCAGTCAAGATTTCA 130  
 QY 1768 CCTCCCCCAGATCCCTAGACAGGAGTGAATGTAATATCCAGAAATTTGGTCTAGTA 1827  
 DB 129 CCTCCCCCAGATCCCTAGACAGGAGTGAATGTAATATCCAGAAATTTGGTCTAGTA 70  
 QY 1828 TAGTACATTTCCCTTCCATTTAAATGTCTTGGGA 1863  
 DB 69 TAGTACATTTCCCTTCCATTTAAATGTCTTGGGA 34

RESULT 12  
 BM669584/c 630 bp mRNA linear EST 27-FEB-2002  
 LOCUS  
 DEFINITION UI-E-DX1-agw-i-19-0-UI.s1 UI-E-DX1 Homo sapiens cDNA clone  
 ACCESSION BM669584  
 VERSION UI-E-DX1-agw-i-19-0-UI 3', mRNA sequence.  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 630)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Forward  
 POLYA=Yes.

## FEATURES

## Source

Location/Qualifiers  
 1. 630  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-E-DX1-agw-i-19-0-UI"  
 /tissue\_type="fetal eyes"  
 /dev\_stage="fetal"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-DX1"  
 /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Ecor I; Site 2: Not I;  
 UI-E-DX1 is a normalized cDNA library containing the  
 following tissue(s): fetal eyes. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an Ecor I  
 adaptor, digested with Not I, and cloned directionally  
 into pT7T3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 AGAATCAAGA. This library was created for the program, Gene  
 Discovery in the Visual System, supported by National Eye  
 Institute (NEI).  
 TAG\_TISSUE=human fetal eyes  
 TAG\_LIB=UI-E-DX1  
 TAG\_SEQ=AGAATCAAGA"

## ORIGIN

Query Match 25.4%; Score 570; DB 4; Length 630;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-267;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 CCGCTGGAGCTGTGATGATGAGAAACATTCGAGATGAGAAATCAACAGGTGAAC 1664  
 DB 587 CCGCTGGAGCTGTGATGATGAGAAACATTCGAGATGAGAAATCAACAGGTGAAC 528  
 QY 1665 TACATAGAGGGAACCAATTAATTTGCTGCTTTTCTTAGAGATGGCCAGCTCATTA 1724  
 DB 527 TACATAGAGGGAACCAATTAATTTGCTGCTTTTCTTAGAGATGGCCAGCTCATTA 468  
 QY 1725 TCACAGAACCCTTCTAGTCTGATGATCCATGACAGATTCACCTCCCAATCCCTA 1784  
 DB 467 TCACAGAACCCTTCTAGTCTGATGATCCATGACAGATTCACCTCCCAATCCCTA 408  
 QY 1785 GACAGGATGGAATGTAATATCCAGAGAATTTGGTCTAGTATAGTACATTTCCCTTC 1844  
 DB 407 GACAGGATGGAATGTAATATCCAGAGAATTTGGTCTAGTATAGTACATTTCCCTTC 348  
 QY 1845 CATTAAATGCTTGGGATATCTGGATCAGTAAATAATATTCAAGGACAGATGTT 1904  
 DB 347 CATTAAATGCTTGGGATATCTGGATCAGTAAATAATATTCAAGGACAGATGTT 288  
 QY 1905 GGAATGTTTAAAGTCCCACTGACACACCTTCTCAAGTATAGTGTCTTCCAGCAAC 1964  
 DB 287 GGAATGTTTAAAGTCCCACTGACACACCTTCTCAAGTATAGTGTCTTCCAGCAAC 228  
 QY 1965 TTGATTTCCCAAGTCTGTGCAATAGCCCGAGATGATGATTCCTTCCAACTTTTAGCA 2024  
 DB 227 TTGATTTCCCAAGTCTGTGCAATAGCCCGAGATGATGATTCCTTCCAACTTTTAGCA 168  
 QY 2025 TATCTCCAACCTTGCAATTTGATTTGGCATATCACTCCGCTTGTCTTCTAGTCTCTCA 2084  
 DB 167 TATCTCCAACCTTGCAATTTGATTTGGCATATCACTCCGCTTGTCTTCTAGTCTCTCA 108